D0128 NP

Figure 1A

```
   1  CCACGCGTCCGCTCAGGTCTATAGGATTAAGAAAGGCAAGCCCAGCAGCCACTACTCACT   60

  61  GACCAGACCTGGCCCAACATGCTGCAGAAATAATTATCAATTAGTATACTTGAGAGACAG   120

 121  CAGCGTGAGGTGGAGAATGGGTTCTAAACTGAATGACAGCTGTTAACAGTTTTTGGCCCT   180

 181  GTTTTTCCTGTCCTGAATCCTCAACTGAGATCCTAGGGATGAGAAACGGGGGAACAGCAC   240

 241  GCCCTACTTGAGAGAATTAGAATTTGAGGCGCTAGGAAGCAAAAGGATCCCAAAGATGGC   300

 301  GACCTGCCAGCCTGGACTGCCAGCGAAGGCCAGAATCGTGCTGTAGCTCTGAACCCACAG   360

 361  CTCCTCTGCCCCTGGCCCATGAGAATTTCAGCTGGAGAGATAGCATGCCCTGGTAAGTGA   420

 421  AGTCCTGCCACTTCGAGACATGGAATCATCTTTCTCATTTGGAGTGATCCTTGCTGTCCT   480
   1                      M  E  S  S  F  S  F  G  V  I  L  A  V  L    14

 481  GGCCTCCCTCATCATTGCTACTAACACACTAGTGGCTGTGGCTGTGCTGCTGTTGATCCA   540
  15   A  S  L  I  I  A  T  N  T  L  V  A  V  A  V  L  L  L  I  H    34

 541  CAAGAATGATGGTGTCAGTCTCTGCTTCACCTTGAATCTGGCTGTGGCTGACACCTTGAT   600
  35   K  N  D  G  V  S  L  C  F  T  L  N  L  A  V  A  D  T  L  I    54

 601  TGGTGTGGCCATCTCTGGCCTACTCACAGACCAGCTCTCCAGCCCTTCTCGGCCCACACA   660
  55   G  V  A  I  S  G  L  L  T  D  Q  L  S  S  P  S  R  P  T  Q    74

 661  GAAGACCCTGTGCAGCCTGCGGATGGCATTTGTCACTTCCTCCGCAGCTGCCTCTGTCCT   720
  75   K  T  L  C  S  L  R  M  A  F  V  T  S  S  A  A  A  S  V  L    94

 721  CACGGTCATGCTGATCACCTTTGACAGGTACCTTGCCATCAAGCAGCCCTTCCGCTACTT   780
  95   T  V  M  L  I  T  F  D  R  Y  L  A  I  K  Q  P  F  R  Y  L   114

 781  GAAGATCATGAGTGGGTTCGTGGCCGGGGCCTGCATTGCCGGGCTGTGGTTAGTGTCTTA   840
 115   K  I  M  S  G  F  V  A  G  A  C  I  A  G  L  W  L  V  S  Y   134

 841  CCTCATTGGCTTCCTCCCACTCGGAATCCCCATGTTCCAGCAGACTGCCTACAAAGGGCA   900
 135   L  I  G  F  L  P  L  G  I  P  M  F  Q  Q  T  A  Y  K  G  Q   154

 901  GTGCAGCTTCTTTGCTGTATTTCACCCTCACTTCGTGCTGACCCTCTCCTGCGTTGGCTT   960
 155   C  S  F  F  A  V  F  H  P  H  F  V  L  T  L  S  C  V  G  F   174
```

D0128 NP

Figure 1B

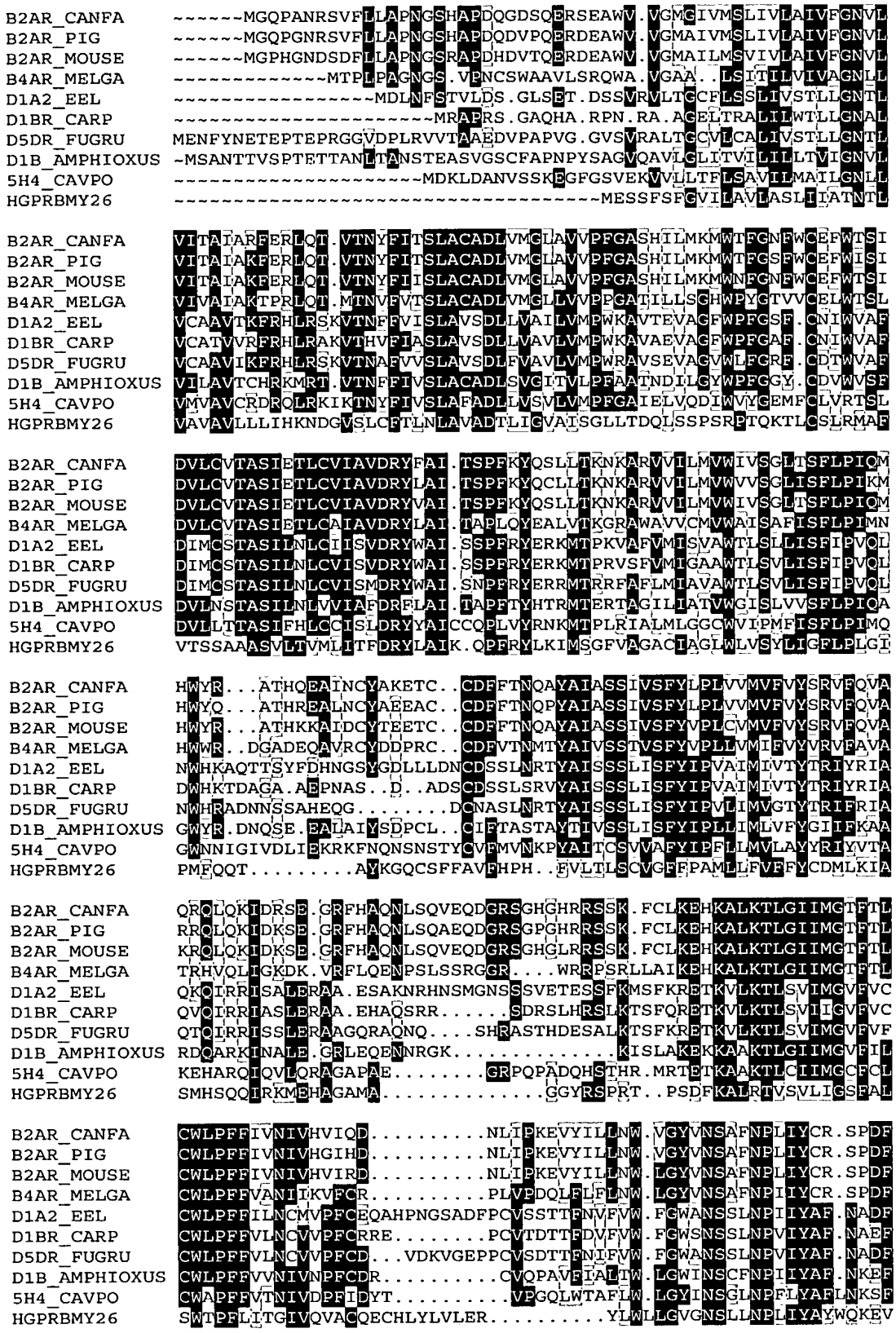
```
961   CTTCCCAGCCATGCTCCTCTTTGTCTTCTTCTACTGCGACATGCTCAAGATTGCCTCCAT  1020
175   F  P  A  M  L  L  F  V  F  F  Y  C  D  M  L  K  I  A  S  M   194

1021  GCACAGCCAGCAGATTCGAAAGATGGAACATGCAGGAGCCATGGCTGGAGGTTATCGATC  1080
195   H  S  Q  Q  I  R  K  M  E  H  A  G  A  M  A  G  G  Y  R  S   214

1081  CCCACGGACTCCCAGCGACTTCAAAGCTCTCCGTACTGTGTCTGTTCTCATTGGGAGCTT  1140
215   P  R  T  P  S  D  F  K  A  L  R  T  V  S  V  L  I  G  S  F   234

1141  TGCTCTATCCTGGACCCCCTTCCTTATCACTGGCATTGTGCAGGTGGCCTGCCAGGAGTG  1200
235   A  L  S  W  T  P  F  L  I  T  G  I  V  Q  V  A  C  Q  E  C   254

1201  TCACCTCTACCTAGTGCTGGAACGGTACCTGTGGCTGCTCGGCGTGGGCAACTCCCTGCT  1260
255   H  L  Y  L  V  L  E  R  Y  L  W  L  L  G  V  G  N  S  L  L   274

1261  CAACCCACTCATCTATGCCTATTGGCAGAAGGAGGTGCGACTGCAGCTCTACCACATGGC  1320
275   N  P  L  I  Y  A  Y  W  Q  K  E  V  R  L  Q  L  Y  H  M  A   294

1321  CCTAGGAGTGAAGAAGGTGCTCACCTCATTCCTCCTCTTTCTCTCGGCCAGGAATTGTGG  1380
295   L  G  V  K  K  V  L  T  S  F  L  L  F  L  S  A  R  N  C  G   314

1381  CCCAGAGAGGCCCAGGGAAAGTTCCTGTCACATCGTCACTATCTCCAGCTCAGAGTTTGA  1440
315   P  E  R  P  R  E  S  S  C  H  I  V  T  I  S  S  S  E  F  D   334

1441  TGGCTAAGACGTCGCTTTGCTTACCAGTCTGGCCCAGAGGAGAAACATGCTTGCTTTCAC  1500
335   G                                                              335

1501  CATAGCAAGCATCGTGTTCCTACAACTGAAGAACTTTTTGACTCTCAAGTGGACGATGGA  1560

1561  ACCCAATATGCCTTGAAATGCTGAGCATCCAGCAAGTACCAGGCCAGCAATAAGGCACAT  1620

1621  TCTTGGATTGTATTGTGAGTTACTGGGAACTAGGTAAAATACGAATAACTGGATTTTGGA  1680

1681  CAAAATTGAAAGCAGGCTCAAACCAATGCCCTCCTTACTGGTGGTTCAAAGCTTAAATCC  1740

1741  TGGCCTTGCTACAAAGGACTGATCTTGCCAAGATAATATAAGCAAAGTGGAATGAAAATT  1800

1801  AAAGTTAATTCTGAAGCCAAGGTCCTTTTAGAAAAAAAAAAAGTAAATTAGCCTGATTTAA  1860

1861  TCATTCCACATTTTAAACATATATCAACATCACATTGTACCCCACGTAATATATACAATT  1920

1921  ATTTGTCAATTAAAAATAAAAAATATATATTTTTAAGTACAGAAAAGCAGGAGGGGAGGA  1980
```

D0128 NP

Figure 1C

```
1981  GAGGCCAGGTGATCAGTGTGTTATTAGGTTCAATCTAAGAAACTCTGCTACCCCTGGGAG  2040

2041  TCAGTATGTGCAATGGAAAAATCACAGGTCTTGAAATCCAACAGACCAGTGTTCAAATGA  2100

2101  TAATTCAGTCATTTAAATTCTCAAACTAGATCTCGCATTCATCAAACCGGGGTAATAATG  2160

2161  CCTACTTTACATGGTTATATTGAAGATTAACTCAGATAATGTATATGTAAATATCTAGTA  2220

2221  AACTACAGCACATTGTTAGTGCTCAAAAAAAAAAAAAAAG  2260
```

Figure 2A


B2AR_CANFA
B2AR_PIG
B2AR_MOUSE
B4AR_MELGA
D1A2_EEL
D1BR_CARP
D5DR_FUGRU
D1B_AMPHIOXUS
5H4_CAVPO
HGPRBMY26

D0128 NP

Figure 2B

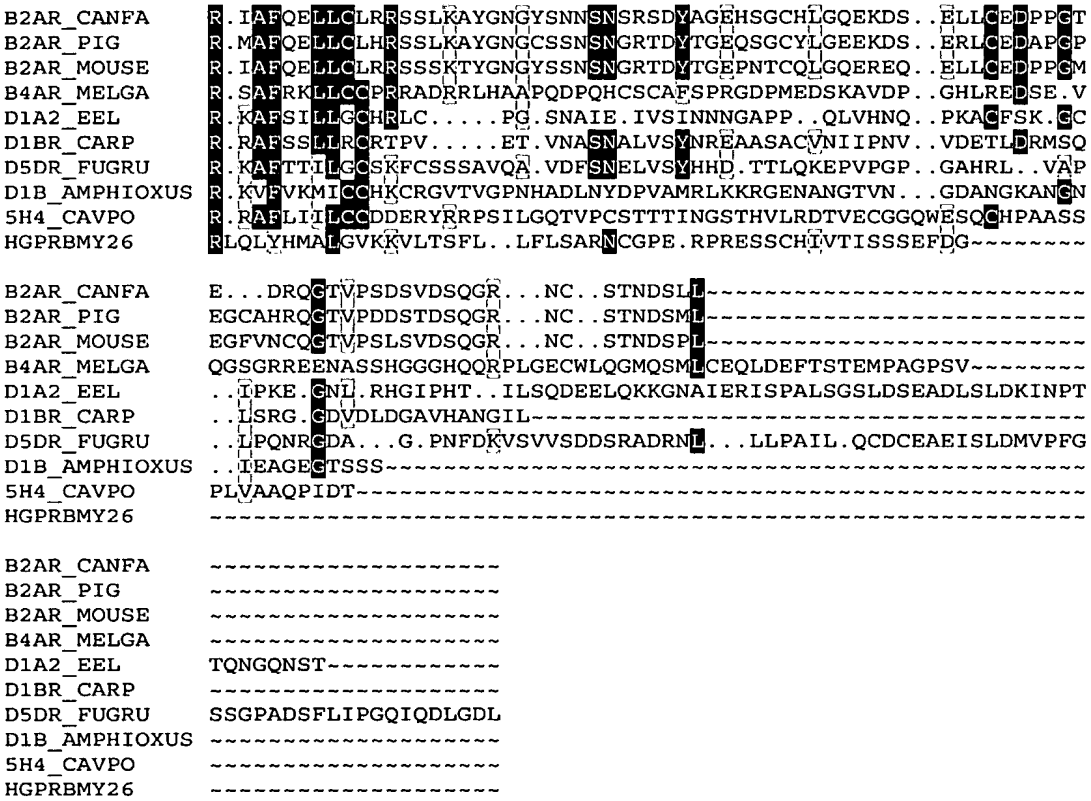
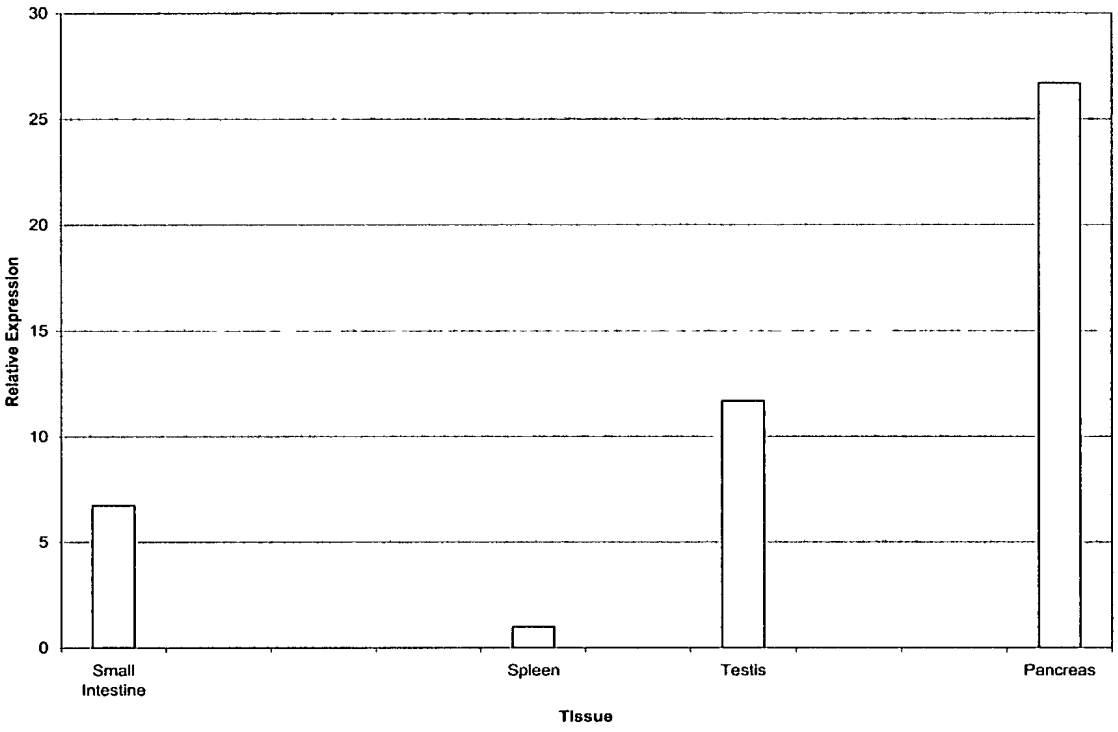


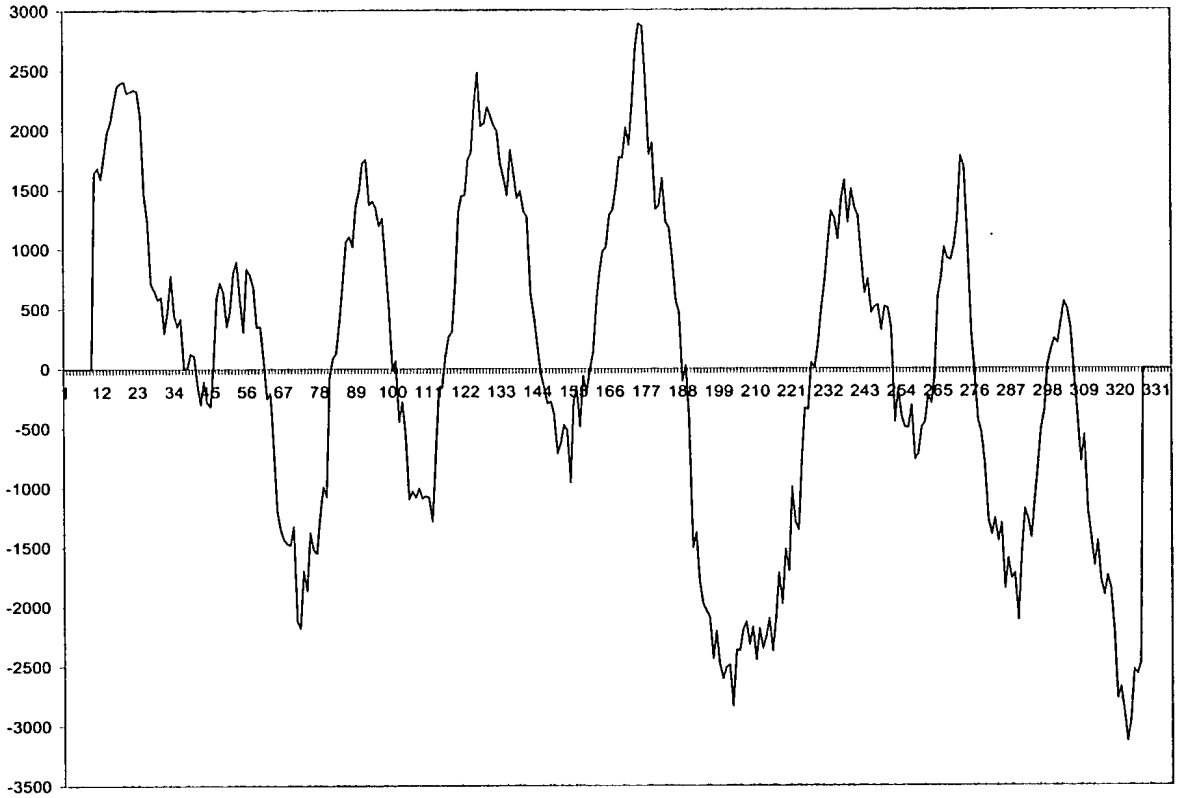
Figure 3



Note: No expression detected in brain, bone marrow, heart, kidney, liver, lung, lymph node, pituitary gland, prostate, spinal cord, or thymus)

D0128 NP

Figure 4

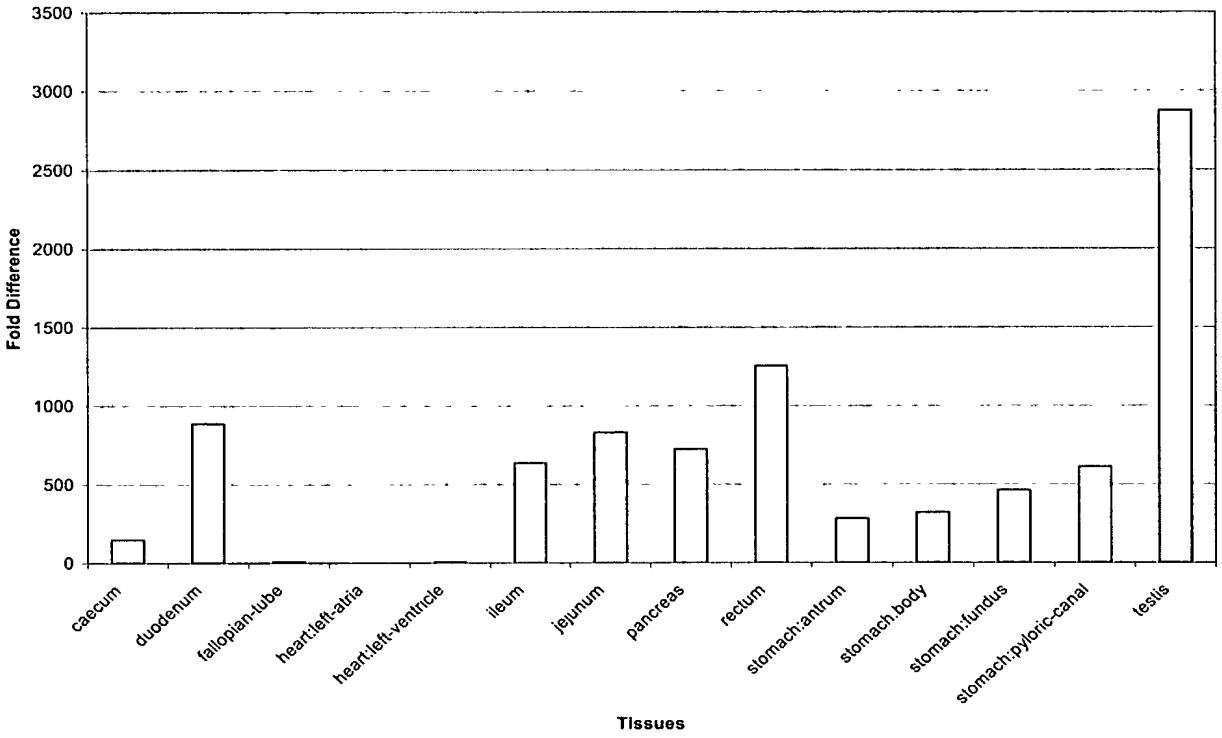


D0128 NP

Figure 5.

Protein	SWISS PROT ID	Identities	Similarities
guinea pig 5-hydroxytryptamine 4 receptor (5-HT-4) protein	gi|O70528	32.18%	40.38%
Amphioxus dopamine D1/beta receptor protein	gi|O96716	26.28%	35.35%
Fugu rubripes D(5)-like dopamine receptor protein	gi|P53454	29.01%	37.35%
carp D1B dopamine receptor protein	gi|O42317	27.22%	35.78%
eel dopamine D1A2 receptor protein	gi|Q98842	29.31%	39.58%
turkey beta-4C adrenergic receptor protein	gi|P43141	29.28%	38.32%
mouse beta-2 adrenergic receptor protein	gi|P18762	27.52%	38.23%
pig beta-2 adrenergic receptor protein	gi|Q28997	29.57%	39.94%
dog beta-2 adrenergic receptor protein	gi|P54833	27.52%	38.53%

Figure 6


3500
3000
2500
2000
1500
1000
500
0
Fold Difference
caecum
duodenum
fallopian-tube
heart:left-atria
heart:left-ventricle
ileum
jejunum
pancreas
rectum
stomach:antrum
stomach:body
stomach:fundus
stomach:pyloric-canal
testis
Tissues

D0128 NP

Figure 7

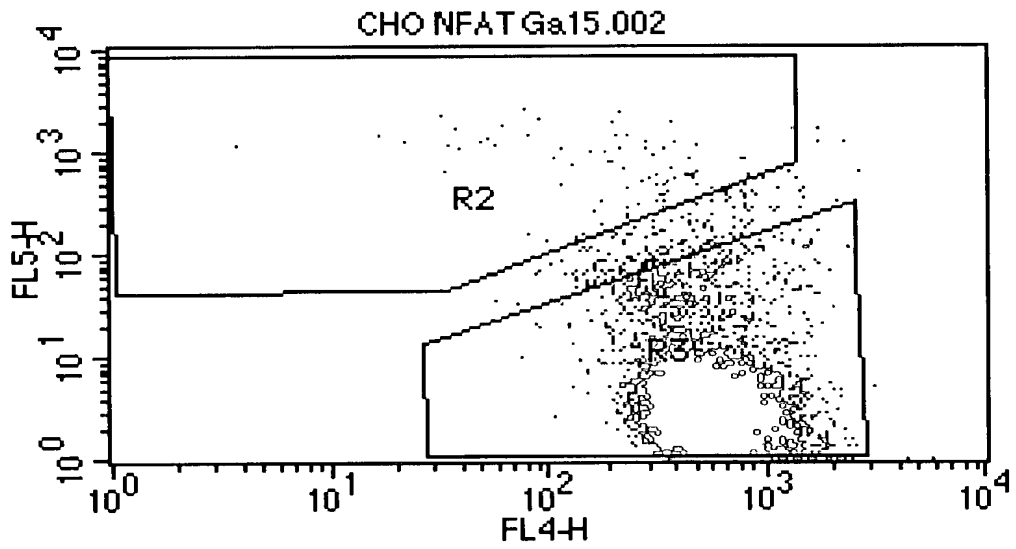
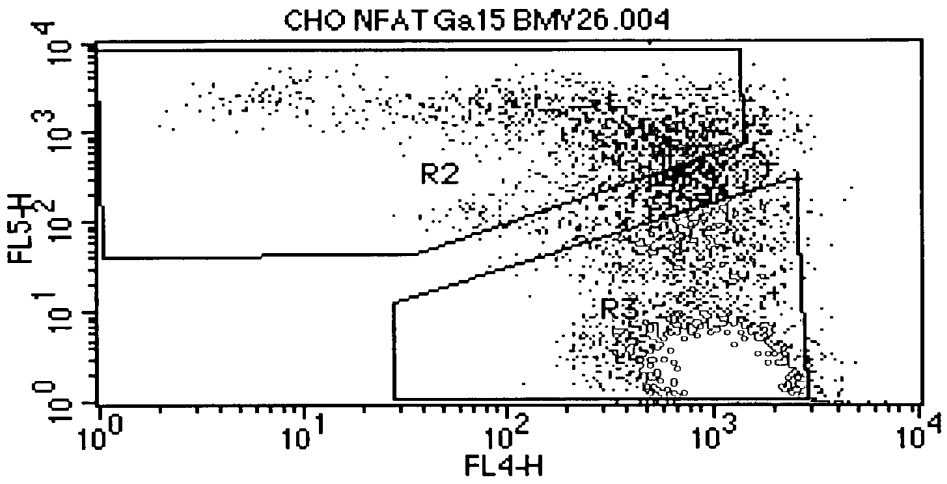


Figure 8



D0128 NP

Figure 9

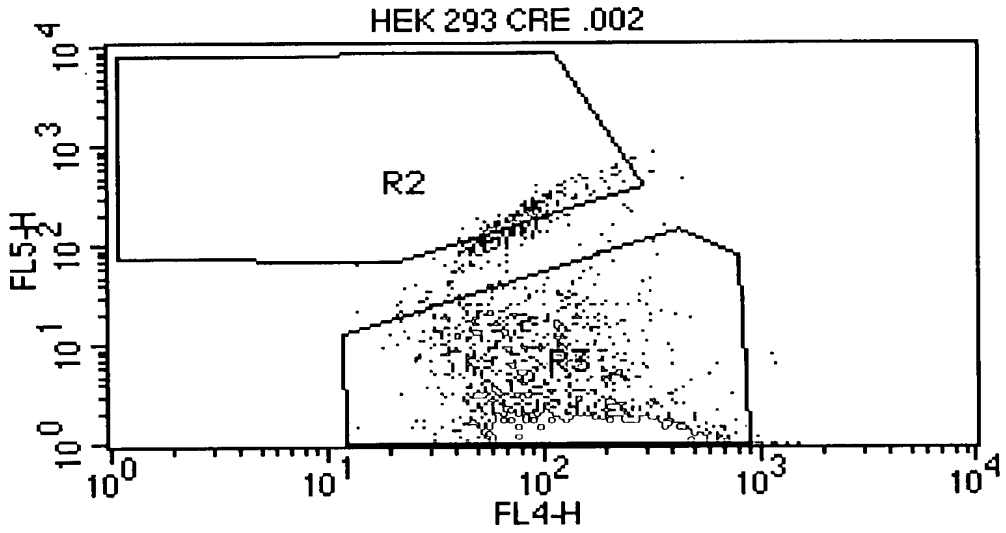
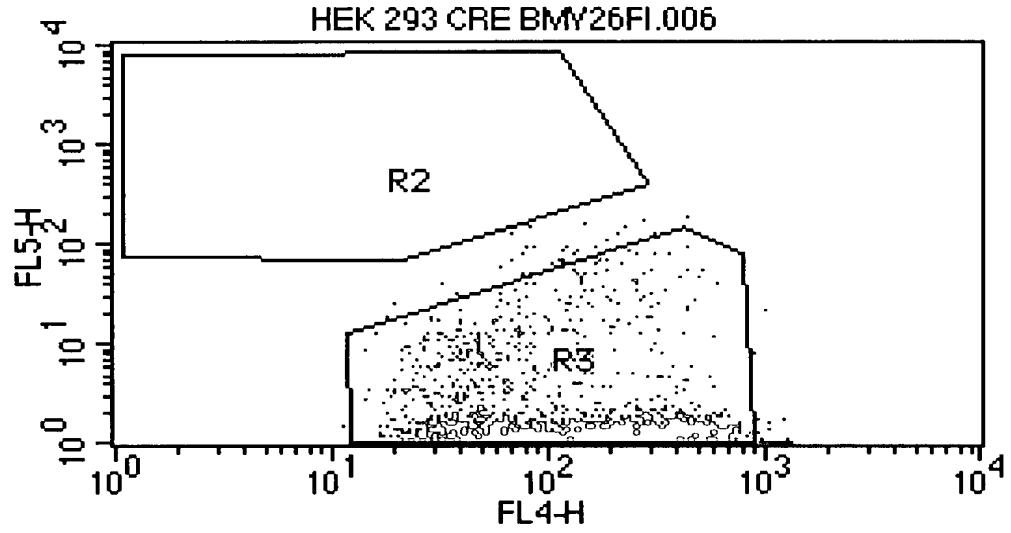


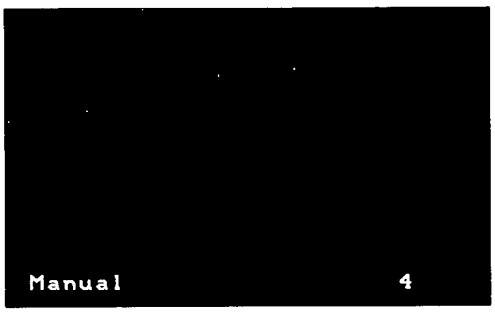
Figure 10

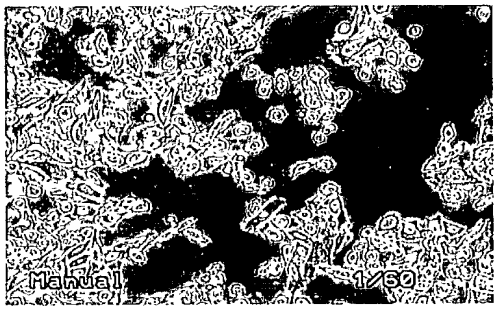


D0128 NP

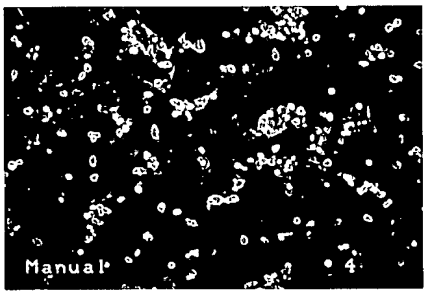
Figure 11

Cho NFAT Ga15 Control (Fluorescent vs. Bright Field)





Cho NFAT Ga15 BMY26 (Fluorescent vs. Bright Field)



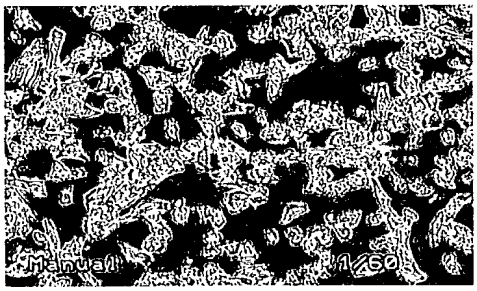
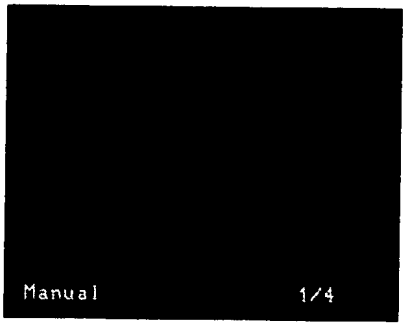
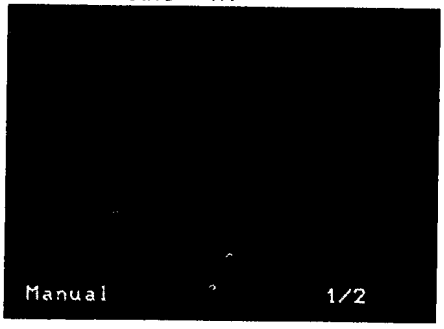


Figure 12

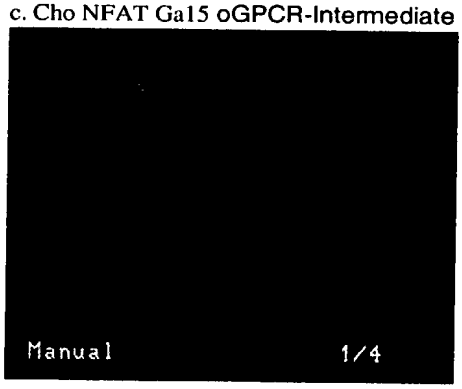
a. Cho NFAT Ga15



b. Cho NFAT Ga15 + T/P



c. Cho NFAT Ga15 oGPCR-Intermediate



d. Cho NFAT Ga15 oGPCR High